

SEQUENCE LISTING

<110> Liang, Yanbin
Woodward, David F.

<120> Human Prostaglandin EP4 Receptor.
Variants and Methods of Using Same

<130> 66872-030

<160> 28

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<212> DNA

<213> Homo sapiens

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<221> CDS

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Leu Asn Ser Pro Val Thr Ile Pro Ala Val Met Phe Ile Phe Gly Val	
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gtg ggc aac ctg gtg gcc atc gtg gtg ctg tgc aag tcg cgc aag gag	144
Val Gly Asn Leu Val Ala Ile Val Val Leu Cys Lys Ser Arg Lys Glu	
35 40 45	

cag aag gag acg acc ttc tac acg ctg gta tgt ggg ctg gct gtc acc	192
Gln Lys Glu Thr Thr Phe Tyr Thr Leu Val Cys Gly Leu Ala Val Thr	
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gac ctg ttg ggc act ttg ttg gtg agc ccg gtg acc atc gcc acg tac	240
Asp Leu Leu Gly Thr Leu Leu Val Ser Pro Val Thr Ile Ala Thr Tyr	
65 70 75 80	

atg aag ggc caa tgg ccc ggg ggc cag ccg ctg tgc gag tac agc acc	288
Met Lys Gly Gln Trp Pro Gly Gly Gln Pro Leu Cys Glu Tyr Ser Thr	
85 90 95	

ttc att ctg ctc ttc ttc agc ctg tcc ggc ctc agc atc atc tgc gcc	336
Phe Ile Leu Leu Phe Phe Ser Leu Ser Gly Leu Ser Ile Ile Cys Ala	
100 105 110	

atg agt gtc gag cgc tac ctg gcc atc aac cat gcc tat ttc tac agc	384
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His	Tyr	Val	Asp	Lys	Arg	Leu	Ala	Gly	Leu	Thr	Leu	Phe	Ala	Val	Tyr		
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gcg	tcc	aac	gtg	ctc	ttt	tgc	gcg	ctg	ccc	aac	atg	ggg	ctc	ggg	agc	480	
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tcg	cgg	ctg	cag	tac	cca	gac	acc	tgg	tgc	ttc	atc	gac	tgg	acc	acc	528	
Ser	Arg	Leu	Gln	Tyr	Pro	Asp	Thr	Trp	Cys	Phe	Ile	Asp	Trp	Thr	Thr		
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aac	gtg	acg	gcg	cac	gcc	gcc	tac	tcc	tac	atg	tac	gcg	ggc	ttc	agc	576	
Asn	Val	Thr	Ala	His	Ala	Ala	Tyr	Ser	Tyr	Met	Tyr	Ala	Gly	Phe	Ser		
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tcc	ttc	ctc	att	ctc	gcc	acc	gtc	ctc	tgc	aac	gtg	ctt	gtg	tgc	ggc	624	
Ser	Phe	Leu	Ile	Leu	Ala	Thr	Val	Leu	Cys	Asn	Val	Leu	Val	Cys	Gly		
		195					200					205					
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Ala	Leu	Leu	Arg	Met	His	Arg	Gln	Phe	Met	Arg	Arg	Thr	Ser	Leu	Gly		
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Thr	Glu	Gln	His	His	Ala	Ala	Ala	Ala	Ala	Ser	Val	Ala	Ser	Arg	Gly		
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cac	ccc	gct	gcc	tcc	cca	gcc	ttg	ccg	cgc	ctc	agc	gac	ttt	cgg	cgc	768	
His	Pro	Ala	Ala	Ser	Pro	Ala	Leu	Pro	Arg	Leu	Ser	Asp	Phe	Arg	Arg		
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Arg	Arg	Ser	Phe	Arg	Arg	Ile	Ala	Gly	Ala	Glu	Ile	Gln	Met	Val	Ile		
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tta	ctc	att	gcc	acc	tcc	ctg	gtg	gtg	ctc	atc	tgc	tcc	atc	ccg	ctc	864	
Leu	Leu	Ile	Ala	Thr	Ser	Leu	Val	Val	Leu	Ile	Cys	Ser	Ile	Pro	Leu		
		275					280					285					
gtg	gca	aac	tgg	aag	tgg	agt	cat	aaa	aca	act	gat	ggg	atg	tca	gat	912	
Val	Ala	Asn	Trp	Lys	Trp	Ser	His	Lys	Thr	Thr	Asp	Gly	Met	Ser	Asp		
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gag	tgt	gaa	gca	cat	cta	tac	ata	caa	gag	aaa	tgc	cac	aaa	ttt	ggg	960	
Glu	Cys	Glu	Ala	His	Leu	Tyr	Ile	Gln	Glu	Lys	Cys	His	Lys	Phe	Gly		
305					310					315					320		
tgc	gag	tat	tcg	tca	acc	agt	tat	atc	agc	caa	gtt	tgg	agc	gag	aag	1008	
Cys	Glu	Tyr	Ser	Ser	Thr	Ser	Tyr	Ile	Ser	Gln	Val	Trp	Ser	Glu	Lys		
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Ser Val Lys Ile Gln Ile Cys Arg Pro Ser Glu Leu Leu Leu *	
340 345 350	

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gcactgtctca gacagtcaaa ggacatcttc tgccatgtca ggccactctc gctccttcat	1234
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 <213> Homo sapiens

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Gln Lys Glu Thr Thr Phe Tyr Thr Leu Val Cys Gly Leu Ala Val Thr	
50 55 60	
Asp Leu Leu Gly Thr Leu Leu Val Ser Pro Val Thr Ile Ala Thr Tyr	
65 70 75 80	
Met Lys Gly Gln Trp Pro Gly Gly Gln Pro Leu Cys Glu Tyr Ser Thr	
85 90 95	
Phe Ile Leu Leu Phe Phe Ser Leu Ser Gly Leu Ser Ile Ile Cys Ala	
100 105 110	
Met Ser Val Glu Arg Tyr Leu Ala Ile Asn His Ala Tyr Phe Tyr Ser	
115 120 125	
His Tyr Val Asp Lys Arg Leu Ala Gly Leu Thr Leu Phe Ala Val Tyr	
130 135 140	
Ala Ser Asn Val Leu Phe Cys Ala Leu Pro Asn Met Gly Leu Gly Ser	
145 150 155 160	
Ser Arg Leu Gln Tyr Pro Asp Thr Trp Cys Phe Ile Asp Trp Thr Thr	
165 170 175	
Asn Val Thr Ala His Ala Ala Tyr Ser Tyr Met Tyr Ala Gly Phe Ser	
180 185 190	
Ser Phe Leu Ile Leu Ala Thr Val Leu Cys Asn Val Leu Val Cys Gly	
195 200 205	
Ala Leu Leu Arg Met His Arg Gln Phe Met Arg Arg Thr Ser Leu Gly	
210 215 220	
Thr Glu Gln His His Ala Ala Ala Ala Ser Val Ala Ser Arg Gly	
225 230 235 240	
His Pro Ala Ala Ser Pro Ala Leu Pro Arg Leu Ser Asp Phe Arg Arg	
245 250 255	
Arg Arg Ser Phe Arg Arg Ile Ala Gly Ala Glu Ile Gln Met Val Ile	
260 265 270	
Leu Leu Ile Ala Thr Ser Leu Val Val Leu Ile Cys Ser Ile Pro Leu	

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Val Ala Asn Trp Lys Trp Ser His Lys Thr Thr Asp Gly Met Ser Asp		
290	295	300
Glu Cys Glu Ala His Leu Tyr Ile Gln Glu Lys Cys His Lys Phe Gly		
305	310	315
Cys Glu Tyr Ser Ser Thr Ser Tyr Ile Ser Gln Val Trp Ser Glu Lys		
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Ser Val Lys Ile Gln Ile Cys Arg Pro Ser Glu Leu Leu Leu		
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Leu Asn Ser Pro Val Thr Ile Pro Ala Val Met Phe Ile Phe Gly Val	
20 25 30	
gtg ggc aac ctg gtg gcc atc gtg gtg ctg tgc aag tcg cgc aag gag	144
Val Gly Asn Leu Val Ala Ile Val Val Leu Cys Lys Ser Arg Lys Glu	
35 40 45	
cag aag gag acg acc ttc tac acg ctg gta tgt ggg ctg gct gtc acc	192
Gln Lys Glu Thr Thr Phe Tyr Thr Leu Val Cys Gly Leu Ala Val Thr	
50 55 60	
gac ctg ttg ggc act ttg ttg gtg agc ccg gtg acc atc gcc acg tac	240
Asp Leu Leu Gly Thr Leu Leu Val Ser Pro Val Thr Ile Ala Thr Tyr	
65 70 75 80	
atg aag ggc caa tgg ccc ggg ggc cag ccg ctg tgc gag tac agc acc	288
Met Lys Gly Gln Trp Pro Gly Gly Gln Pro Leu Cys Glu Tyr Ser Thr	
85 90 95	
ttc att ctg ctc ttc ttc agc ctg tcc ggc ctc agc atc atc tgc gcc	336
Phe Ile Leu Leu Phe Phe Ser Leu Ser Gly Leu Ser Ile Ile Cys Ala	
100 105 110	
atg agt gtc gag cgc tac ctg gcc atc aac cat gcc tat ttc tac agc	384
Met Ser Val Glu Arg Tyr Leu Ala Ile Asn His Ala Tyr Phe Tyr Ser	
115 120 125	
cac tac gtg gac aag cga ttg gcg ggc ctc acg ctc ttt gca gtc tat	432
His Tyr Val Asp Lys Arg Leu Ala Gly Leu Thr Leu Phe Ala Val Tyr	
130 135 140	

gcg tcc aac gtg ctc ttt tgc gcg ctg ccc aac atg ggt ctc ggt agc Ala Ser Asn Val Leu Phe Cys Ala Leu Pro Asn Met Gly Leu Gly Ser 145 150 155 160	480
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aac gtg acg gcg cac gcc gcc tac tcc tac atg tac gcg ggc ttc agc Asn Val Thr Ala His Ala Ala Tyr Ser Tyr Met Tyr Ala Gly Phe Ser 180 185 190	576
tcc ttc ctc att ctc gcc acc gtc ctc tgc aac gtg ctt gtg tgc ggc Ser Phe Leu Ile Leu Ala Thr Val Leu Cys Asn Val Leu Val Cys Gly 195 200 205	624
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acc gag cag cac cac gcg gcc gcg gcc gcc tcg gtt gcc tcc cgg ggc Thr Glu Gln His His Ala Ala Ala Ala Ala Ser Val Ala Ser Arg Gly 225 230 235 240	720
cac ccc gct gcc tcc cca gcc ttg ccg cgc ctc agc gac ttt cgg cgc His Pro Ala Ala Ser Pro Ala Leu Pro Arg Leu Ser Asp Phe Arg Arg 245 250 255	768
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tta ctc att gcc acc tcc ctg gtg gtg ctc atc tgc tcc atc ccg ctc Leu Leu Ile Ala Thr Ser Leu Val Val Leu Ile Cys Ser Ile Pro Leu 275 280 285	864
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<210> 4
 <211> 326
 <212> PRT
 <213> Homo sapiens

<400> 4

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Gln Lys Glu Thr Thr Phe Tyr Thr Leu Val Cys Gly Leu Ala Val Thr	
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Asp Leu Leu Gly Thr Leu Leu Val Ser Pro Val Thr Ile Ala Thr Tyr	
65 70 75 80	
Met Lys Gly Gln Trp Pro Gly Gly Gln Pro Leu Cys Glu Tyr Ser Thr	
85 90 95	
Phe Ile Leu Leu Phe Phe Ser Leu Ser Gly Leu Ser Ile Ile Cys Ala	
100 105 110	
Met Ser Val Glu Arg Tyr Leu Ala Ile Asn His Ala Tyr Phe Tyr Ser	
115 120 125	
His Tyr Val Asp Lys Arg Leu Ala Gly Leu Thr Leu Phe Ala Val Tyr	
130 135 140	
Ala Ser Asn Val Leu Phe Cys Ala Leu Pro Asn Met Gly Leu Gly Ser	
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Ser Arg Leu Gln Tyr Pro Asp Thr Trp Cys Phe Ile Asp Trp Thr Thr	
165 170 175	
Asn Val Thr Ala His Ala Ala Tyr Ser Tyr Met Tyr Ala Gly Phe Ser	
180 185 190	
Ser Phe Leu Ile Leu Ala Thr Val Leu Cys Asn Val Leu Val Cys Gly	
195 200 205	
Ala Leu Leu Arg Met His Arg Gln Phe Met Arg Arg Thr Ser Leu Gly	
210 215 220	
Thr Glu Gln His His Ala Ala Ala Ala Ser Val Ala Ser Arg Gly	
225 230 235 240	
His Pro Ala Ala Ser Pro Ala Leu Pro Arg Leu Ser Asp Phe Arg Arg	
245 250 255	
Arg Arg Ser Phe Arg Arg Ile Ala Gly Ala Glu Ile Gln Met Val Ile	
260 265 270	
Leu Leu Ile Ala Thr Ser Leu Val Val Leu Ile Cys Ser Ile Pro Leu	
275 280 285	
Val Phe Pro Lys Leu Gln Met Lys Asn Leu Tyr His Ser Ala Thr Tyr	
290 295 300	
Arg Val Ala Ile Gly Ala Ser Ile Arg Gln Pro Val Ile Ser Ala Lys	
305 310 315 320	
Phe Gly Ala Arg Ser Gln	
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<212> DNA
 <213> Homo sapiens

<220>
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 Leu Asn Ser Pro Val Thr Ile Pro Ala Val Met Phe Ile Phe Gly Val
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gtg ggc aac ctg gtg gcc atc gtg gtg ctg tgc aag tcc cgc aag gag 144
 Val Gly Asn Leu Val Ala Ile Val Val Leu Cys Lys Ser Arg Lys Glu
 35 40 45

cag aag gag acg acc ttc tac acg ctg gta tgt ggg ctg gct gtc acc 192
 Gln Lys Glu Thr Thr Phe Tyr Thr Leu Val Cys Gly Leu Ala Val Thr
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gac ctg ttg ggc act ttg ttg gtg agc ccg gtg acc atc gcc acg tac 240
 Asp Leu Leu Gly Thr Leu Leu Val Ser Pro Val Thr Ile Ala Thr Tyr
 65 70 75 80

atg aag ggc caa tgg ccc ggg ggc cag ccg ctg tgc gag tac agc acc 288
 Met Lys Gly Gln Trp Pro Gly Gly Gln Pro Leu Cys Glu Tyr Ser Thr
 85 90 95

ttc att ctg ctc ttc ttc agc ctg tcc ggc ctc agc atc atc tgc gcc 336
 Phe Ile Leu Leu Phe Phe Ser Leu Ser Gly Leu Ser Ile Ile Cys Ala
 100 105 110

atg agt gtc gag cgc tac ctg gcc atc aac cat gcc tat ttc tac agc 384
 Met Ser Val Glu Arg Tyr Leu Ala Ile Asn His Ala Tyr Phe Tyr Ser
 115 120 125

cac tac gtg gac aag cga ttg gcg ggc ctc acg ctc ttt gca gtc tat 432
 His Tyr Val Asp Lys Arg Leu Ala Gly Leu Thr Leu Phe Ala Val Tyr
 130 135 140

gcg tcc aac gtg ctc ttt tgc gcg ctg ccc aac atg ggt ctc ggt agc 480
 Ala Ser Asn Val Leu Phe Cys Ala Leu Pro Asn Met Gly Leu Gly Ser
 145 150 155 160

tcc cgg ctg cag tac cca gac acc tgg tgc ttc atc gac tgg acc acc 528
 Ser Arg Leu Gln Tyr Pro Asp Thr Trp Cys Phe Ile Asp Trp Thr Thr
 165 170 175

aac gtg acg gcg cac gcc gcc tac tcc tac atg tac gcg ggc ttc agc 576
 Asn Val Thr Ala His Ala Ala Tyr Ser Tyr Met Tyr Ala Gly Phe Ser
 180 185 190

tcc ttc ctc att ctc gcc acc gtc ctc tgc aac gtg ctt gtg tgc ggc	624
Ser Phe Leu Ile Leu Ala Thr Val Leu Cys Asn Val Leu Val Cys Gly	
195 200 205	
gcg ctg ctc cgc atg cac cgc cag ttc atg cgc cgc acc tcg ctg ggc	672
Ala Leu Leu Arg Met His Arg Gln Phe Met Arg Arg Thr Ser Leu Gly	
210 215 220	
acc gag cag cac cac gcg gcc gcg gcc gcc tcg gtt gcc tcc cgg ggc	720
Thr Glu Gln His His Ala Ala Ala Ala Ala Ser Val Ala Ser Arg Gly	
225 230 235 240	
cac ccc gct gcc tcc cca gcc ttg ccg cgc ctc agc gac ttt cgg cgc	768
His Pro Ala Ala Ser Pro Ala Leu Pro Arg Leu Ser Asp Phe Arg Arg	
245 250 255	
cgc cgg agc ttc cgc cgc atc gcg ggc gcc gag atc cag atg gtc atc	816
Arg Arg Ser Phe Arg Arg Ile Ala Gly Ala Glu Ile Gln Met Val Ile	
260 265 270	
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Leu Leu Ile Ala Thr Ser Leu Val Val Leu Ile Cys Ser Ile Pro Leu	
275 280 285	
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Val Ala Asn Trp Lys Trp Ser His Lys Thr Thr Asp Gly Met Ser Asp	
290 295 300	
gag tgt gaa gca cat cta tac ata caa gag aaa tgc cac aaa ttt ggg	960
Glu Cys Glu Ala His Leu Tyr Ile Gln Glu Lys Cys His Lys Phe Gly	
305 310 315 320	
tat gac tat gac aga atc tga aagactggat ttgttcaaataaatttggt	1011
Tyr Asp Tyr Asp Arg Ile *	
325	

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aatttatatc attctgcaac ttacagggtg gctataggtg cgagtattcg tcaaccagtt	1191
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 <212> PRT
 <213> Homo sapiens

<400> 6

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			20					25					30		
Val	Gly	Asn	Leu	Val	Ala	Ile	Val	Val	Leu	Cys	Lys	Ser	Arg	Lys	Glu
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Gln	Lys	Glu	Thr	Thr	Phe	Tyr	Thr	Leu	Val	Cys	Gly	Leu	Ala	Val	Thr
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Asp	Leu	Leu	Gly	Thr	Leu	Leu	Val	Ser	Pro	Val	Thr	Ile	Ala	Thr	Tyr
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Met	Lys	Gly	Gln	Trp	Pro	Gly	Gly	Gln	Pro	Leu	Cys	Glu	Tyr	Ser	Thr
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Phe	Ile	Leu	Leu	Phe	Phe	Ser	Leu	Ser	Gly	Leu	Ser	Ile	Ile	Cys	Ala
			100					105					110		
Met	Ser	Val	Glu	Arg	Tyr	Leu	Ala	Ile	Asn	His	Ala	Tyr	Phe	Tyr	Ser
		115					120						125		
His	Tyr	Val	Asp	Lys	Arg	Leu	Ala	Gly	Leu	Thr	Leu	Phe	Ala	Val	Tyr
	130						135				140				
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Ser	Arg	Leu	Gln	Tyr	Pro	Asp	Thr	Trp	Cys	Phe	Ile	Asp	Trp	Thr	Thr
			165					170						175	
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Ser	Phe	Leu	Ile	Leu	Ala	Thr	Val	Leu	Cys	Asn	Val	Leu	Val	Cys	Gly
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Ala	Leu	Leu	Arg	Met	His	Arg	Gln	Phe	Met	Arg	Arg	Thr	Ser	Leu	Gly
210						215						220			
Thr	Glu	Gln	His	His	Ala	Ala	Ala	Ala	Ala	Ser	Val	Ala	Ser	Arg	Gly
225					230					235					240
His	Pro	Ala	Ala	Ser	Pro	Ala	Leu	Pro	Arg	Leu	Ser	Asp	Phe	Arg	Arg
			245						250					255	
Arg	Arg	Ser	Phe	Arg	Arg	Ile	Ala	Gly	Ala	Glu	Ile	Gln	Met	Val	Ile
		260						265					270		
Leu	Leu	Ile	Ala	Thr	Ser	Leu	Val	Val	Leu	Ile	Cys	Ser	Ile	Pro	Leu
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Val	Ala	Asn	Trp	Lys	Trp	Ser	His	Lys	Thr	Thr	Asp	Gly	Met	Ser	Asp
	290					295					300				
Glu	Cys	Glu	Ala	His	Leu	Tyr	Ile	Gln	Glu	Lys	Cys	His	Lys	Phe	Gly
305					310					315					320
Tyr	Asp	Tyr	Asp	Arg	Ile										
				325											

<210> 7

<211> 183

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(183)

<400> 7

gca aac tgg aag tgg agt cat aaa aca act gat ggg atg tca gat gag 48
 Ala Asn Trp Lys Trp Ser His Lys Thr Thr Asp Gly Met Ser Asp Glu
 1 5 10 15

tgt gaa gca cat cta tac ata caa gag aaa tgc cac aaa ttt ggg tgc 96
 Cys Glu Ala His Leu Tyr Ile Gln Glu Lys Cys His Lys Phe Gly Cys
 20 25 30

gag tat tcg tca acc agt tat atc agc caa gtt tgg agc gag aag tca 144
 Glu Tyr Ser Ser Thr Ser Tyr Ile Ser Gln Val Trp Ser Glu Lys Ser
 35 40 45

gta aaa atc cag att tgc agg cca tcc gaa ttg ctt ctg 183
 Val Lys Ile Gln Ile Cys Arg Pro Ser Glu Leu Leu Leu
 50 55 60

<210> 8
 <211> 61
 <212> PRT
 <213> Homo sapiens

<400> 8
 Ala Asn Trp Lys Trp Ser His Lys Thr Thr Asp Gly Met Ser Asp Glu
 1 5 10 15
 Cys Glu Ala His Leu Tyr Ile Gln Glu Lys Cys His Lys Phe Gly Cys
 20 25 30
 Glu Tyr Ser Ser Thr Ser Tyr Ile Ser Gln Val Trp Ser Glu Lys Ser
 35 40 45
 Val Lys Ile Gln Ile Cys Arg Pro Ser Glu Leu Leu Leu
 50 55 60

<210> 9
 <211> 111
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(111)

<400> 9
 ttt ccc aag ctg caa atg aag aat tta tat cat tct gca act tac agg 48
 Phe Pro Lys Leu Gln Met Lys Asn Leu Tyr His Ser Ala Thr Tyr Arg
 1 5 10 15

gta gct ata ggt gcg agt att cgt caa cca gtt ata tca gcc aag ttt 96
 Val Ala Ile Gly Ala Ser Ile Arg Gln Pro Val Ile Ser Ala Lys Phe
 20 25 30

gga gcg aga agt cag 111
 Gly Ala Arg Ser Gln
 35

<210> 10
 <211> 37
 <212> PRT
 <213> Homo sapiens

<400> 10
 Phe Pro Lys Leu Gln Met Lys Asn Leu Tyr His Ser Ala Thr Tyr Arg
 1 5 10 15
 Val Ala Ile Gly Ala Ser Ile Arg Gln Pro Val Ile Ser Ala Lys Phe
 20 25 30
 Gly Ala Arg Ser Gln
 35

<210> 11
 <211> 111
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(111)

<400> 11
 gca aac tgg aag tgg agt cat aaa aca act gat ggg atg tca gat gag. 48
 Ala Asn Trp Lys Trp Ser His Lys Thr Thr Asp Gly Met Ser Asp Glu
 1 5 10 15
 tgt gaa gca cat cta tac ata caa gag aaa tgc cac aaa ttt ggg tat 96
 Cys Glu Ala His Leu Tyr Ile Gln Glu Lys Cys His Lys Phe Gly Tyr
 20 25 30
 gac tat gac aga atc 111
 Asp Tyr Asp Arg Ile
 35

<210> 12
 <211> 37
 <212> PRT
 <213> Homo sapiens

<400> 12
 Ala Asn Trp Lys Trp Ser His Lys Thr Thr Asp Gly Met Ser Asp Glu
 1 5 10 15
 Cys Glu Ala His Leu Tyr Ile Gln Glu Lys Cys His Lys Phe Gly Tyr
 20 25 30
 Asp Tyr Asp Arg Ile
 35

<210> 13
 <211> 27
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
<222> (1)...(27)

<400> 13
atc ccg ctc gtg gca aac tgg aag tgg
Ile Pro Leu Val Ala Asn Trp Lys Trp
1 5

27

<210> 14
<211> 9
<212> PRT
<213> Homo sapiens

<400> 14
Ile Pro Leu Val Ala Asn Trp Lys Trp
1 5

<210> 15
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(27)

<400> 15
atc ccg ctc gtg ttt ccc aag ctg caa
Ile Pro Leu Val Phe Pro Lys Leu Gln
1 5

27

<210> 16
<211> 9
<212> PRT
<213> Homo sapiens

<400> 16
Ile Pro Leu Val Phe Pro Lys Leu Gln
1 5

<210> 17
<211> 1470
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1470)

<400> 17
atg tcc act ccc ggg gtc aat tgg tcc gcc tcc ttg agc ccc gac cgg
Met Ser Thr Pro Gly Val Asn Ser Ser Ala Ser Leu Ser Pro Asp Arg
1 5 10 15

48

ctg aac agc cca gtg acc atc ccg gcg gtg atg ttc atc ttc ggg gtg	96
Leu Asn Ser Pro Val Thr Ile Pro Ala Val Met Phe Ile Phe Gly Val	
20 25 30	
gtg ggc aac ctg gtg gcc atc gtg gtg ctg tgc aag tcg cgc aag gag	144
Val Gly Asn Leu Val Ala Ile Val Val Leu Cys Lys Ser Arg Lys Glu	
35 40 45	
cag aag gag acg acc ttc tac acg ctg gta tgt ggg ctg gct gtc acc	192
Gln Lys Glu Thr Thr Phe Tyr Thr Leu Val Cys Gly Leu Ala Val Thr	
50 55 60	
gac ctg ttg ggc act ttg ttg gtg agc ccg gtg acc atc gcc acg tac	240
Asp Leu Leu Gly Thr Leu Leu Val Ser Pro Val Thr Ile Ala Thr Tyr	
65 70 75 80	
atg aag ggc caa tgg ccc ggg ggc cag ccg ctg tgc gag tac agc acc	288
Met Lys Gly Gln Trp Pro Gly Gly Gln Pro Leu Cys Glu Tyr Ser Thr	
85 90 95	
ttc att ctg ctc ttc ttc agc ctg tcc ggc ctc agc atc atc tgc gcc	336
Phe Ile Leu Leu Phe Phe Ser Leu Ser Gly Leu Ser Ile Ile Cys Ala	
100 105 110	
atg agt gtc gag cgc tac ctg gcc atc aac cat gcc tat ttc tac agc	384
Met Ser Val Glu Arg Tyr Leu Ala Ile Asn His Ala Tyr Phe Tyr Ser	
115 120 125	
cac tac gtg gac aag cga ttg gcg ggc ctc acg ctc ttt gca gtc tat	432
His Tyr Val Asp Lys Arg Leu Ala Gly Leu Thr Leu Phe Ala Val Tyr	
130 135 140	
gcg tcc aac gtg ctc ttt tgc gcg ctg ccc aac atg ggt ctc ggt agc	480
Ala Ser Asn Val Leu Phe Cys Ala Leu Pro Asn Met Gly Leu Gly Ser	
145 150 155 160	
tcg cgg ctg cag tac cca gac acc tgg tgc ttc atc gac tgg acc acc	528
Ser Arg Leu Gln Tyr Pro Asp Thr Trp Cys Phe Ile Asp Trp Thr Thr	
165 170 175	
aac gtg acg gcg cac gcc gcc tac tcc tac atg tac gcg ggc ttc agc	576
Asn Val Thr Ala His Ala Ala Tyr Ser Tyr Met Tyr Ala Gly Phe Ser	
180 185 190	
tcc ttc ctc att ctc gcc acc gtc ctc tgc aac gtg ctt gtg tgc ggc	624
Ser Phe Leu Ile Leu Ala Thr Val Leu Cys Asn Val Leu Val Cys Gly	
195 200 205	
gcg ctg ctc cgc atg cac cgc cag ttc atg cgc cgc acc tcg ctg ggc	672
Ala Leu Leu Arg Met His Arg Gln Phe Met Arg Arg Thr Ser Leu Gly	
210 215 220	
acc gag cag cac cac gcg gcc gcg gcc gcc tcg gtt gcc tcc cgg ggc	720
Thr Glu Gln His His Ala Ala Ala Ala Ala Ser Val Ala Ser Arg Gly	

225	230	235	240	
cac ccc gct gcc tcc cca gcc ttg ccg cgc ctc agc gac ttt cgg cgc				768
His Pro Ala Ala Ser Pro Ala Leu Pro Arg Leu Ser Asp Phe Arg Arg				
	245	250	255	
cgc cgg agc ttc cgc cgc atc gcg ggc gcc gag atc cag atg gtc atc				816
Arg Arg Ser Phe Arg Arg Ile Ala Gly Ala Glu Ile Gln Met Val Ile				
	260	265	270	
tta ctc att gcc acc tcc ctg gtg gtg ctc atc tgc tcc atc ccg ctc				864
Leu Leu Ile Ala Thr Ser Leu Val Val Leu Ile Cys Ser Ile Pro Leu				
	275	280	285	
gtg gtg cga gta ttc gtc aac cag tta tat cag cca agt ttg gag cga				912
Val Val Arg Val Phe Val Asn Gln Leu Tyr Gln Pro Ser Leu Glu Arg				
	290	295	300	
gaa gtc agt aaa aat cca gat ttg cag gcc atc cga att gct tct gtg				960
Glu Val Ser Lys Asn Pro Asp Leu Gln Ala Ile Arg Ile Ala Ser Val				
	305	310	315	320
aac ccc atc cta gac ccc tgg ata tat atc ctc ctg aga aag aca gtg				1008
Asn Pro Ile Leu Asp Pro Trp Ile Tyr Ile Leu Leu Arg Lys Thr Val				
	325	330	335	
ctc agt aaa gca ata gag aag atc aaa tgc ctc ttc tgc cgc att ggc				1056
Leu Ser Lys Ala Ile Glu Lys Ile Lys Cys Leu Phe Cys Arg Ile Gly				
	340	345	350	
ggg tcc cgc agg gag cgc tcc gga cag cac tgc tca gac agt caa agg				1104
Gly Ser Arg Arg Glu Arg Ser Gly Gln His Cys Ser Asp Ser Gln Arg				
	355	360	365	
aca tct tct gcc atg tca ggc cac tct cgc tcc ttc atc tcc cgg gag				1152
Thr Ser Ser Ala Met Ser Gly His Ser Arg Ser Phe Ile Ser Arg Glu				
	370	375	380	
ctg aag gag atc agc agt aca tct cag acc ctc ctg cca gac ctc tca				1200
Leu Lys Glu Ile Ser Ser Thr Ser Gln Thr Leu Leu Pro Asp Leu Ser				
	385	390	395	400
ctg cca gac ctc agt gaa aat ggc ctt gga ggc agg aat ttg ctt cca				1248
Leu Pro Asp Leu Ser Glu Asn Gly Leu Gly Gly Arg Asn Leu Leu Pro				
	405	410	415	
ggt gtg cct ggc atg ggc ctg gcc cag gaa gac acc acc tca ctg agg				1296
Gly Val Pro Gly Met Gly Leu Ala Gln Glu Asp Thr Thr Ser Leu Arg				
	420	425	430	
act ttg cga ata tca gag acc tca gac tct tca cag ggt cag gac tca				1344
Thr Leu Arg Ile Ser Glu Thr Ser Asp Ser Ser Gln Gly Gln Asp Ser				
	435	440	445	
gag agt gtc tta ctg gtg gat gag gct ggt ggg agc ggc agg gct ggg				1392

Glu Ser Val Leu Leu Val Asp Glu Ala Gly Gly Ser Gly Arg Ala Gly
 450 455 460

cct gcc cct aag ggg agc tcc ctg caa gtc aca ttt ccc agt gaa aca 1440
 Pro Ala Pro Lys Gly Ser Ser Leu Gln Val Thr Phe Pro Ser Glu Thr
 465 470 475 480

ctg aac tta tca gaa aaa tgt ata taa tag 1470
 Leu Asn Leu Ser Glu Lys Cys Ile * *
 485

<210> 18
 <211> 488
 <212> PRT
 <213> Homo sapiens

<400> 18
 Met Ser Thr Pro Gly Val Asn Ser Ser Ala Ser Leu Ser Pro Asp Arg
 1 5 10 15
 Leu Asn Ser Pro Val Thr Ile Pro Ala Val Met Phe Ile Phe Gly Val
 20 25 30
 Val Gly Asn Leu Val Ala Ile Val Val Leu Cys Lys Ser Arg Lys Glu
 35 40 45
 Gln Lys Glu Thr Thr Phe Tyr Thr Leu Val Cys Gly Leu Ala Val Thr
 50 55 60
 Asp Leu Leu Gly Thr Leu Leu Val Ser Pro Val Thr Ile Ala Thr Tyr
 65 70 75 80
 Met Lys Gly Gln Trp Pro Gly Gly Gln Pro Leu Cys Glu Tyr Ser Thr
 85 90 95
 Phe Ile Leu Leu Phe Phe Ser Leu Ser Gly Leu Ser Ile Ile Cys Ala
 100 105 110
 Met Ser Val Glu Arg Tyr Leu Ala Ile Asn His Ala Tyr Phe Tyr Ser
 115 120 125
 His Tyr Val Asp Lys Arg Leu Ala Gly Leu Thr Leu Phe Ala Val Tyr
 130 135 140
 Ala Ser Asn Val Leu Phe Cys Ala Leu Pro Asn Met Gly Leu Gly Ser
 145 150 155 160
 Ser Arg Leu Gln Tyr Pro Asp Thr Trp Cys Phe Ile Asp Trp Thr Thr
 165 170 175
 Asn Val Thr Ala His Ala Ala Tyr Ser Tyr Met Tyr Ala Gly Phe Ser
 180 185 190
 Ser Phe Leu Ile Leu Ala Thr Val Leu Cys Asn Val Leu Val Cys Gly
 195 200 205
 Ala Leu Leu Arg Met His Arg Gln Phe Met Arg Arg Thr Ser Leu Gly
 210 215 220
 Thr Glu Gln His His Ala Ala Ala Ala Ser Val Ala Ser Arg Gly
 225 230 235 240
 His Pro Ala Ala Ser Pro Ala Leu Pro Arg Leu Ser Asp Phe Arg Arg
 245 250 255
 Arg Arg Ser Phe Arg Arg Ile Ala Gly Ala Glu Ile Gln Met Val Ile
 260 265 270
 Leu Leu Ile Ala Thr Ser Leu Val Val Leu Ile Cys Ser Ile Pro Leu
 275 280 285
 Val Val Arg Val Phe Val Asn Gln Leu Tyr Gln Pro Ser Leu Glu Arg

290		295		300	
Glu Val Ser Lys Asn Pro Asp Leu Gln Ala Ile Arg Ile Ala Ser Val					
305		310		315	320
Asn Pro Ile Leu Asp Pro Trp Ile Tyr Ile Leu Leu Arg Lys Thr Val					
	325		330		335
Leu Ser Lys Ala Ile Glu Lys Ile Lys Cys Leu Phe Cys Arg Ile Gly					
	340		345		350
Gly Ser Arg Arg Glu Arg Ser Gly Gln His Cys Ser Asp Ser Gln Arg					
	355		360		365
Thr Ser Ser Ala Met Ser Gly His Ser Arg Ser Phe Ile Ser Arg Glu					
	370		375		380
Leu Lys Glu Ile Ser Ser Thr Ser Gln Thr Leu Leu Pro Asp Leu Ser					
385		390		395	400
Leu Pro Asp Leu Ser Glu Asn Gly Leu Gly Gly Arg Asn Leu Leu Pro					
	405		410		415
Gly Val Pro Gly Met Gly Leu Ala Gln Glu Asp Thr Thr Ser Leu Arg					
	420		425		430
Thr Leu Arg Ile Ser Glu Thr Ser Asp Ser Ser Gln Gly Gln Asp Ser					
	435		440		445
Glu Ser Val Leu Leu Val Asp Glu Ala Gly Gly Ser Gly Arg Ala Gly					
	450		455		460
Pro Ala Pro Lys Gly Ser Ser Leu Gln Val Thr Phe Pro Ser Glu Thr					
465		470		475	480
Leu Asn Leu Ser Glu Lys Cys Ile					
	485				

<210> 19
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 19
 agatggtcatt cttactcatt g

21

<210> 20
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 20
 gatgtactgc tgatctcctt c

21

<210> 21
 <211> 20
 <212> DNA
 <213> Homo sapiens

<400> 21
 tcccgcctcgt gtttcccaag

20

<210> 22
<211> 20
<212> DNA
<213> Homo sapiens

<400> 22
gtagctatag gtgcgagtat

20

<210> 23
<211> 20
<212> DNA
<213> Homo sapiens

<400> 23
taacataaaa tttcccaagc

20

<210> 24
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 24
ttactcattg ccaacctccc t

21

<210> 25
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 25
cccaaatttg tggcatttct

20

<210> 26
<211> 22
<212> DNA
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<220>
<223> primer

<400> 26
ctaccctgta agttgcagaa tg

22

<210> 27
<211> 20
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<220>

<223> primer

<400> 27

tttccaagc tgcaaatgaa

20

<210> 28

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 28

tatccagggg tctaggatgg

20